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<110> Duke University
Arcasoy, Murat O.
Haroon, Zishan A.

<120> Use of Novel Cytokine Receptors as Biomarkers and Therapeutic
Targets in Human Cancer

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ggctccacg gctcgtggtg cggcgctt ctggtgttcg ctgcctacag ccgacacgtc 480
gagcttcgtg cccctagagt tgcgcgtcac agcagcctcc ggcgctccgc gatatacccg 540
tgtcatccac atcaatgaag tagtgctcct agacgcccc gtggggctgg tggcgcggtt 600
ggctgacgag agcggccacg tagtggtgcg ctggctcccg ccgcctgaga caccatgac 660
gtctcacatc cgctacgagg tggacgtctc ggccggcaac ggcgcaggga gcgtacagag 720
ggtggagatc ctggagggcc gcaccgagtg tgtgctgagc aacctgcggg gccggacgcg 780
ctacaccttc gccgtccgcg cgcgtatggc tgagccgagc ttcggcggt tctggagcgc 840
ctggctcgag cctgtgtcgc tgctgacgcc tagcgacctg gacccctca tctgacgct 900
ctccctcatc ctcgtggtca tctggtgct gctgaccgtg ctgcgctgc tctccaccg 960
ccgggctctg aagcagaaga tctggcctgg catcccgagc ccagagagcg agtttgaagg 1020
cctcttcacc accacaagg gtaacttcca gctgtggctg taccagaatg atggtgct 1080
gtggtggagc ccctgcaccc cttcacgga ggaccacct gcttccctgg aagtccctc 1140
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gctggagcca gtgggcagt agcatgcca ggatacctat ctggtgctgg acaaatggtt 1260
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agccgctgag cctctgcccc ccagctatgt ggcttgctct taggacacca ggctgcagat 1680
gatcagggat ccaatatgac tcagagaacc agtgcagact caagacttat ggaacaggga 1740
tggcgaggcc tctctcagga gcaggggcat tgctgatttt gtctgccc aa tccatcctgc 1800
tcaggaaacc acaaccttgc agtattttta aatatgtata gtttttttat atgtatagtt 1860
ttttt 1865

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<210> 4
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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1) .. (855)

<223> EpoR Isoform 1, intron 6 insert

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<400> 4

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Met Asp His Leu Gly Ala Ser Leu Trp Pro Gln Val Gly Ser Leu Cys	
1 5 10 15	
ctc ctg ctc gct ggg gcc gcc tgg gcg ccc ccg cct aac ctc ccg gac	96
Leu Leu Leu Ala Gly Ala Ala Trp Ala Pro Pro Pro Asn Leu Pro Asp	
20 25 30	
ccc aag ttc gag agc aaa gcg gcc ttg ctg gcg gcc cgg ggg ccc gaa	144
Pro Lys Phe Glu Ser Lys Ala Ala Leu Leu Ala Ala Arg Gly Pro Glu	
35 40 45	
gag ctt ctg tgc ttc acc gag cgg ttg gag gac ttg gtg tgt ttc tgg	192
Glu Leu Leu Cys Phe Thr Glu Arg Leu Glu Asp Leu Val Cys Phe Trp	
50 55 60	
gag gaa gcg gcg agc gct ggg gtg ggc ccg ggc aac tac agc ttc tcc	240
Glu Glu Ala Ala Ser Ala Gly Val Gly Pro Gly Asn Tyr Ser Phe Ser	
65 70 75 80	
tac cag ctc gag gat gag cca tgg aag ctg tgt cgc ctg cac cag gct	288
Tyr Gln Leu Glu Asp Glu Pro Trp Lys Leu Cys Arg Leu His Gln Ala	
85 90 95	
ccc acg gct cgt ggt gcg gtg cgc ttc tgg tgt tcg ctg cct aca gcc	336
Pro Thr Ala Arg Gly Ala Val Arg Phe Trp Cys Ser Leu Pro Thr Ala	
100 105 110	
gac acg tcg agc ttc gtg ccc cta gag ttg cgc gtc aca gca gcc tcc	384
Asp Thr Ser Ser Phe Val Pro Leu Glu Leu Arg Val Thr Ala Ala Ser	
115 120 125	
ggc gct ccg cga tat cac cgt gtc atc cac atc aat gaa gta gtg ctc	432
Gly Ala Pro Arg Tyr His Arg Val Ile His Ile Asn Glu Val Val Leu	
130 135 140	
cta gac gcc ccc gtg ggg ctg gtg gcg cgg ttg gct gac gag agc ggc	480
Leu Asp Ala Pro Val Gly Leu Val Ala Arg Leu Ala Asp Glu Ser Gly	
145 150 155 160	
cac gta gtg ttg cgc tgg ctc ccg ccg cct gag aca ccc atg acg tct	528
His Val Val Leu Arg Trp Leu Pro Pro Pro Glu Thr Pro Met Thr Ser	
165 170 175	
cac atc cgc tac gag gtg gac gtc tcg gcc ggc aac ggc gca ggg agc	576
His Ile Arg Tyr Glu Val Asp Val Ser Ala Gly Asn Gly Ala Gly Ser	
180 185 190	
gta cag agg gtg gag atc ctg gag ggc cgc acc gag tgt gtg ctg agc	624
Val Gln Arg Val Glu Ile Leu Glu Gly Arg Thr Glu Cys Val Leu Ser	
195 200 205	
aac ctg cgg ggc cgg acg cgc tac acc ttc gcc gtc cgc gcg cgt atg	672
Asn Leu Arg Gly Arg Thr Arg Tyr Thr Phe Ala Val Arg Ala Arg Met	
210 215 220	
gct gag ccg agc ttc ggc ggc ttc tgg agc gcc tgg tcg gag cct gtg	720
Ala Glu Pro Ser Phe Gly Gly Phe Trp Ser Ala Trp Ser Glu Pro Val	

225				230				235				240				
tcg	ctg	ctg	acg	cct	agc	gac	ctg	gac	ccc	ctc	atc	ctg	acg	ctc	tcc	768
Ser	Leu	Leu	Thr	Pro	Ser	Asp	Leu	Asp	Pro	Leu	Ile	Leu	Thr	Leu	Ser	
				245				250				255				
ctc	atc	ctc	gtg	gtc	atc	ctg	gtg	ctg	ctg	acc	gtg	ctc	gcg	ctg	ctc	816
Leu	Ile	Leu	Val	Val	Ile	Leu	Val	Leu	Leu	Thr	Val	Leu	Ala	Leu	Leu	
				260				265				270				
tcc	cac	cgc	cgg	atg	gtc	agg	gaa	ggc	tcc	agg	agg	agg	tga			858
Ser	His	Arg	Arg	Met	Val	Arg	Glu	Gly	Ser	Arg	Arg	Arg				
275				280				285								

Met 1	Asp	His	Leu	Gly 5	Ala	Ser	Leu	Trp	Pro	Gln	Val	Gly	Ser	Leu	Cys
Leu	Leu	Leu	Ala 20	Gly	Ala	Ala	Trp	Ala 25	Pro	Pro	Pro	Asn	Leu 30	Pro	Asp
Pro	Lys	Phe 35	Glu	Ser	Lys	Ala	Ala 40	Leu	Leu	Ala	Ala	Arg 45	Gly	Pro	Glu
Glu 50	Leu	Leu	Cys	Phe	Thr	Glu 55	Arg	Leu	Glu	Asp	Leu 60	Val	Cys	Phe	Trp
Glu 65	Glu	Ala	Ala	Ser	Ala 70	Gly	Val	Gly	Pro	Gly 75	Asn	Tyr	Ser	Phe	Ser 80
Tyr	Gln	Leu	Glu	Asp 85	Glu	Pro	Trp	Lys 90	Leu	Cys	Arg	Leu	His 95	Gln	Ala
Pro	Thr	Ala	Arg 100	Gly	Ala	Val	Arg	Phe 105	Trp	Cys	Ser	Leu	Pro 110	Thr	Ala
Asp	Thr	Ser 115	Ser	Phe	Val	Pro	Leu 120	Glu	Leu	Arg	Val	Thr 125	Ala	Ala	Ser
Gly 130	Ala	Pro	Arg	Tyr	His	Arg 135	Val	Ile	His	Ile	Asn 140	Glu	Val	Val	Leu
Leu 145	Asp	Ala	Pro	Val	Gly 150	Leu	Val	Ala	Arg	Leu 155	Ala	Asp	Glu	Ser	Gly 160

His Val Val Leu Arg Trp Leu Pro Pro Pro Glu Thr Pro Met Thr Ser
165 170 175

His Ile Arg Tyr Glu Val Asp Val Ser Ala Gly Asn Gly Ala Gly Ser
180 185 190

Val Gln Arg Val Glu Ile Leu Glu Gly Arg Thr Glu Cys Val Leu Ser
195 200 205

Asn Leu Arg Gly Arg Thr Arg Tyr Thr Phe Ala Val Arg Ala Arg Met
210 215 220

Ala Glu Pro Ser Phe Gly Gly Phe Trp Ser Ala Trp Ser Glu Pro Val
225 230 235 240

Ser Leu Leu Thr Pro Ser Asp Leu Asp Pro Leu Ile Leu Thr Leu Ser
245 250 255

Leu Ile Leu Val Val Ile Leu Val Leu Leu Thr Val Leu Ala Leu Leu
260 265 270

Ser His Arg Arg Met Val Arg Glu Gly Ser Arg Arg Arg
275 280 285

<210> 6
<211> 954
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(951)
<223> EpoR Isoform 2, intron 7 insert

<400> 6
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ctc ctg ctc gct ggg gcc gcc tgg gcg ccc ccg cct aac ctc ccg gac 96
Leu Leu Leu Ala Gly Ala Ala Trp Ala Pro Pro Pro Asn Leu Pro Asp
20 25 30
ccc aag ttc gag agc aaa gcg gcc ttg ctg gcg gcc cgg ggg ccc gaa 144
Pro Lys Phe Glu Ser Lys Ala Ala Leu Leu Ala Ala Arg Gly Pro Glu
35 40 45
gag ctt ctg tgc ttc acc gag cgg ttg gag gac ttg gtg tgt ttc tgg 192
Glu Leu Leu Cys Phe Thr Glu Arg Leu Glu Asp Leu Val Cys Phe Trp
50 55 60

gag gaa gcg gcg agc gct ggg gtg ggc ccg ggc aac tac agc ttc tcc Glu Glu Ala Ala Ser Ala Gly Val Gly Pro Gly Asn Tyr Ser Phe Ser 65 70 75 80	240
tac cag ctc gag gat gag cca tgg aag ctg tgt cgc ctg cac cag gct Tyr Gln Leu Glu Asp Glu Pro Trp Lys Leu Cys Arg Leu His Gln Ala 85 90 95	288
ccc acg gct cgt ggt gcg gtg cgc ttc tgg tgt tcg ctg cct aca gcc Pro Thr Ala Arg Gly Ala Val Arg Phe Trp Cys Ser Leu Pro Thr Ala 100 105 110	336
gac acg tcg agc ttc gtg ccc cta gag ttg cgc gtc aca gca gcc tcc Asp Thr Ser Ser Phe Val Pro Leu Glu Leu Arg Val Thr Ala Ala Ser 115 120 125	384
ggc gct ccg cga tat cac cgt gtc atc cac atc aat gaa gta gtg ctc Gly Ala Pro Arg Tyr His Arg Val Ile His Ile Asn Glu Val Val Leu 130 135 140	432
cta gac gcc ccc gtg ggg ctg gtg gcg cgg ttg gct gac gag agc ggc Leu Asp Ala Pro Val Gly Leu Val Ala Arg Leu Ala Asp Glu Ser Gly 145 150 155 160	480
cac gta gtg ttg cgc tgg ctc ccg ccg cct gag aca ccc atg acg tct His Val Val Leu Arg Trp Leu Pro Pro Pro Glu Thr Pro Met Thr Ser 165 170 175	528
cac atc cgc tac gag gtg gac gtc tcg gcc ggc aac ggc gca ggg agc His Ile Arg Tyr Glu Val Asp Val Ser Ala Gly Asn Gly Ala Gly Ser 180 185 190	576
gta cag agg gtg gag atc ctg gag ggc cgc acc gag tgt gtg ctg agc Val Gln Arg Val Glu Ile Leu Glu Gly Arg Thr Glu Cys Val Leu Ser 195 200 205	624
aac ctg cgg ggc cgg acg cgc tac acc ttc gcc gtc cgc gcg cgt atg Asn Leu Arg Gly Arg Thr Arg Tyr Thr Phe Ala Val Arg Ala Arg Met 210 215 220	672
gct gag ccg agc ttc ggc ggc ttc tgg agc gcc tgg tcg gag cct gtg Ala Glu Pro Ser Phe Gly Gly Phe Trp Ser Ala Trp Ser Glu Pro Val 225 230 235 240	720
tcg ctg ctg acg cct agc gac ctg gac ccc ctc atc ctg acg ctc tcc Ser Leu Leu Thr Pro Ser Asp Leu Asp Pro Leu Ile Leu Thr Leu Ser 245 250 255	768
ctc atc ctc gtg gtc atc ctg gtg ctg ctg acc gtg ctc gcg ctg ctc Leu Ile Leu Val Val Ile Leu Val Leu Leu Thr Val Leu Ala Leu Leu 260 265 270	816
tcc cac cgc cgg gct ctg aag cag aag atc tgg cct ggc atc ccg agc Ser His Arg Arg Ala Leu Lys Gln Lys Ile Trp Pro Gly Ile Pro Ser 275 280 285	864
cca gag agc gag ttt gaa ggc ctc ttc acc acc cac aag ggt aac ttc Pro Glu Ser Glu Phe Glu Gly Leu Phe Thr Thr His Lys Gly Asn Phe 290 295 300	912
cag gtt ggt gct att tct tca gct gtg gct gta cca gaa tga	954

Gln Val Gly Ala Ile Ser Ser Ala Val Ala Val Pro Glu
 305 310 315

<210> 7
 <211> 317
 <212> PRT
 <213> Homo sapiens

<400> 7

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Leu Leu Leu Ala Gly Ala Ala Trp Ala Pro Pro Pro Asn Leu Pro Asp
 20 25 30

Pro Lys Phe Glu Ser Lys Ala Ala Leu Leu Ala Ala Arg Gly Pro Glu
 35 40 45

Glu Leu Leu Cys Phe Thr Glu Arg Leu Glu Asp Leu Val Cys Phe Trp
 50 55 60

Glu Glu Ala Ala Ser Ala Gly Val Gly Pro Gly Asn Tyr Ser Phe Ser
 65 70 75 80

Tyr Gln Leu Glu Asp Glu Pro Trp Lys Leu Cys Arg Leu His Gln Ala
 85 90 95

Pro Thr Ala Arg Gly Ala Val Arg Phe Trp Cys Ser Leu Pro Thr Ala
 100 105 110

Asp Thr Ser Ser Phe Val Pro Leu Glu Leu Arg Val Thr Ala Ala Ser
 115 120 125

Gly Ala Pro Arg Tyr His Arg Val Ile His Ile Asn Glu Val Val Leu
 130 135 140

Leu Asp Ala Pro Val Gly Leu Val Ala Arg Leu Ala Asp Glu Ser Gly
 145 150 155 160

His Val Val Leu Arg Trp Leu Pro Pro Pro Glu Thr Pro Met Thr Ser
 165 170 175

His Ile Arg Tyr Glu Val Asp Val Ser Ala Gly Asn Gly Ala Gly Ser
 180 185 190

Val Gln Arg Val Glu Ile Leu Glu Gly Arg Thr Glu Cys Val Leu Ser
 195 200 205

Asn Leu Arg Gly Arg Thr Arg Tyr Thr Phe Ala Val Arg Ala Arg Met
 210 215 220

Ala Glu Pro Ser Phe Gly Gly Phe Trp Ser Ala Trp Ser Glu Pro Val
 225 230 235 240

Ser Leu Leu Thr Pro Ser Asp Leu Asp Pro Leu Ile Leu Thr Leu Ser
 245 250 255

Leu Ile Leu Val Val Ile Leu Val Leu Leu Thr Val Leu Ala Leu Leu
 260 265 270

Ser His Arg Arg Ala Leu Lys Gln Lys Ile Trp Pro Gly Ile Pro Ser
 275 280 285

Pro Glu Ser Glu Phe Glu Gly Leu Phe Thr Thr His Lys Gly Asn Phe
 290 295 300

Gln Val Gly Ala Ile Ser Ser Ala Val Ala Val Pro Glu
 305 310 315

<210> 8
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 <213> Homo sapiens

<220>
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 <222> (1)..(984)
 <223> EpOR Isoform 3, intron 7 unspliced

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ctc ctg ctc gct ggg gcc gcc tgg gcg ccc ccg cct aac ctc ccg gac 96
 Leu Leu Leu Ala Gly Ala Ala Trp Ala Pro Pro Pro Asn Leu Pro Asp
 20 25 30

ccc aag ttc gag agc aaa gcg gcc ttg ctg gcg gcc cgg ggg ccc gaa 144
 Pro Lys Phe Glu Ser Lys Ala Ala Leu Leu Ala Ala Arg Gly Pro Glu
 35 40 45

gag ctt ctg tgc ttc acc gag cgg ttg gag gac ttg gtg tgt ttc tgg 192
 Glu Leu Leu Cys Phe Thr Glu Arg Leu Glu Asp Leu Val Cys Phe Trp
 50 55 60

gag gaa gcg gcg agc gct ggg gtg ggc ccg ggc aac tac agc ttc tcc 240
 Glu Glu Ala Ala Ser Ala Gly Val Gly Pro Gly Asn Tyr Ser Phe Ser
 65 70 75 80

tac cag ctc gag gat gag cca tgg aag ctg tgt cgc ctg cac cag gct Tyr Gln Leu Glu Asp Glu Pro Trp Lys Leu Cys Arg Leu His Gln Ala 85 90 95	288
ccc acg gct cgt ggt gcg gtg cgc ttc tgg tgt tcg ctg cct aca gcc Pro Thr Ala Arg Gly Ala Val Arg Phe Trp Cys Ser Leu Pro Thr Ala 100 105 110	336
gac acg tcg agc ttc gtg ccc cta gag ttg cgc gtc aca gca gcc tcc Asp Thr Ser Ser Phe Val Pro Leu Glu Leu Arg Val Thr Ala Ala Ser 115 120 125	384
ggc gct ccg cga tat cac cgt gtc atc cac atc aat gaa gta gtg ctc Gly Ala Pro Arg Tyr His Arg Val Ile His Ile Asn Glu Val Val Leu 130 135 140	432
cta gac gcc ccc gtg ggg ctg gtg gcg cgg ttg gct gac gag agc ggc Leu Asp Ala Pro Val Gly Leu Val Ala Arg Leu Ala Asp Glu Ser Gly 145 150 155 160	480
cac gta gtg ttg cgc tgg ctc ccg ccg cct gag aca ccc atg acg tct His Val Val Leu Arg Trp Leu Pro Pro Pro Glu Thr Pro Met Thr Ser 165 170 175	528
cac atc cgc tac gag gtg gac gtc tcg gcc ggc aac ggc gca ggg agc His Ile Arg Tyr Glu Val Asp Val Ser Ala Gly Asn Gly Ala Gly Ser 180 185 190	576
gta cag agg gtg gag atc ctg gag ggc cgc acc gag tgt gtg ctg agc Val Gln Arg Val Glu Ile Leu Glu Gly Arg Thr Glu Cys Val Leu Ser 195 200 205	624
aac ctg cgg ggc cgg acg cgc tac acc ttc gcc gtc cgc gcg cgt atg Asn Leu Arg Gly Arg Thr Arg Tyr Thr Phe Ala Val Arg Ala Arg Met 210 215 220	672
gct gag ccg agc ttc ggc ggc ttc tgg agc gcc tgg tcg gag cct gtg Ala Glu Pro Ser Phe Gly Gly Phe Trp Ser Ala Trp Ser Glu Pro Val 225 230 235 240	720
tcg ctg ctg acg cct agc gac ctg gac ccc ctc atc ctg acg ctc tcc Ser Leu Leu Thr Pro Ser Asp Leu Asp Pro Leu Ile Leu Thr Leu Ser 245 250 255	768
ctc atc ctc gtg gtc atc ctg gtg ctg ctg acc gtg ctc gcg ctg ctc Leu Ile Leu Val Val Ile Leu Val Leu Leu Thr Val Leu Ala Leu Leu 260 265 270	816
tcc cac cgc cgg gct ctg aag cag aag atc tgg cct ggc atc ccg agc Ser His Arg Arg Ala Leu Lys Gln Lys Ile Trp Pro Gly Ile Pro Ser 275 280 285	864
cca gag agc gag ttt gaa ggc ctc ttc acc acc cac aag ggt aac ttc Pro Glu Ser Glu Phe Glu Gly Leu Phe Thr Thr His Lys Gly Asn Phe 290 295 300	912
cag gta ggt ggc ctg gtt gtc ccc tca gtg cct ggg ctt ccc tgc ttc Gln Val Gly Gly Leu Val Val Pro Ser Val Pro Gly Leu Pro Cys Phe 305 310 315 320	960

ttg cag cca aac tgc agg cct ctc tga
 Leu Gln Pro Asn Cys Arg Pro Leu
 325

987

<210> 9
 <211> 328
 <212> PRT
 <213> Homo sapiens

<400> 9

Met Asp His Leu Gly Ala Ser Leu Trp Pro Gln Val Gly Ser Leu Cys
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Leu Leu Leu Ala Gly Ala Ala Trp Ala Pro Pro Pro Asn Leu Pro Asp
 20 25 30

Pro Lys Phe Glu Ser Lys Ala Ala Leu Leu Ala Ala Arg Gly Pro Glu
 35 40 45

Glu Leu Leu Cys Phe Thr Glu Arg Leu Glu Asp Leu Val Cys Phe Trp
 50 55 60

Glu Glu Ala Ala Ser Ala Gly Val Gly Pro Gly Asn Tyr Ser Phe Ser
 65 70 75 80

Tyr Gln Leu Glu Asp Glu Pro Trp Lys Leu Cys Arg Leu His Gln Ala
 85 90 95

Pro Thr Ala Arg Gly Ala Val Arg Phe Trp Cys Ser Leu Pro Thr Ala
 100 105 110

Asp Thr Ser Ser Phe Val Pro Leu Glu Leu Arg Val Thr Ala Ala Ser
 115 120 125

Gly Ala Pro Arg Tyr His Arg Val Ile His Ile Asn Glu Val Val Leu
 130 135 140

Leu Asp Ala Pro Val Gly Leu Val Ala Arg Leu Ala Asp Glu Ser Gly
 145 150 155 160

His Val Val Leu Arg Trp Leu Pro Pro Pro Glu Thr Pro Met Thr Ser
 165 170 175

His Ile Arg Tyr Glu Val Asp Val Ser Ala Gly Asn Gly Ala Gly Ser
 180 185 190

Val Gln Arg Val Glu Ile Leu Glu Gly Arg Thr Glu Cys Val Leu Ser

195 200 205

Asn Leu Arg Gly Arg Thr Arg Tyr Thr Phe Ala Val Arg Ala Arg Met
210 215 220

Ala Glu Pro Ser Phe Gly Gly Phe Trp Ser Ala Trp Ser Glu Pro Val
225 230 235 240

Ser Leu Leu Thr Pro Ser Asp Leu Asp Pro Leu Ile Leu Thr Leu Ser
245 250 255

Leu Ile Leu Val Val Ile Leu Val Leu Leu Thr Val Leu Ala Leu Leu
260 265 270

Ser His Arg Arg Ala Leu Lys Gln Lys Ile Trp Pro Gly Ile Pro Ser
275 280 285

Pro Glu Ser Glu Phe Glu Gly Leu Phe Thr Thr His Lys Gly Asn Phe
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Gln Val Gly Gly Leu Val Val Pro Ser Val Pro Gly Leu Pro Cys Phe
305 310 315 320

Leu Gln Pro Asn Cys Arg Pro Leu
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<210> 10
<211> 804
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(801)
<223> EpoR Isoform 4, intron 5 unspliced

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ctc ctg ctc gct ggg gcc gcc tgg gcg ccc ccg cct aac ctc ccg gac 96
Leu Leu Leu Ala Gly Ala Ala Trp Ala Pro Pro Pro Asn Leu Pro Asp
20 25 30

ccc aag ttc gag agc aaa gcg gcc ttg ctg gcg gcc cgg ggg ccc gaa 144
Pro Lys Phe Glu Ser Lys Ala Ala Leu Leu Ala Ala Arg Gly Pro Glu
35 40 45

gag ctt ctg tgc ttc acc gag cgg ttg gag gac ttg gtg tgt ttc tgg 192
Glu Leu Leu Cys Phe Thr Glu Arg Leu Glu Asp Leu Val Cys Phe Trp

50	55	60	
gag gaa gcg gcg agc gct ggg gtg ggc ccg ggc aac tac agc ttc tcc			240
Glu Glu Ala Ala Ser Ala Gly Val Gly Pro Gly Asn Tyr Ser Phe Ser			
65	70	75	80
tac cag ctc gag gat gag cca tgg aag ctg tgt cgc ctg cac cag gct			288
Tyr Gln Leu Glu Asp Glu Pro Trp Lys Leu Cys Arg Leu His Gln Ala			
	85	90	95
ccc acg gct cgt ggt gcg gtg cgc ttc tgg tgt tcg ctg cct aca gcc			336
Pro Thr Ala Arg Gly Ala Val Arg Phe Trp Cys Ser Leu Pro Thr Ala			
	100	105	110
gac acg tcg agc ttc gtg ccc cta gag ttg cgc gtc aca gca gcc tcc			384
Asp Thr Ser Ser Phe Val Pro Leu Glu Leu Arg Val Thr Ala Ala Ser			
	115	120	125
ggc gct ccg cga tat cac cgt gtc atc cac atc aat gaa gta gtg ctc			432
Gly Ala Pro Arg Tyr His Arg Val Ile His Ile Asn Glu Val Val Leu			
	130	135	140
cta gac gcc ccc gtg ggg ctg gtg gcg cgg ttg gct gac gag agc ggc			480
Leu Asp Ala Pro Val Gly Leu Val Ala Arg Leu Ala Asp Glu Ser Gly			
	145	150	155
cac gta gtg ttg cgc tgg ctc ccg ccg cct gag aca ccc atg acg tct			528
His Val Val Leu Arg Trp Leu Pro Pro Pro Glu Thr Pro Met Thr Ser			
	165	170	175
cac atc cgc tac gag gtg gac gtc tcg gcc ggc aac ggc gca ggg agc			576
His Ile Arg Tyr Glu Val Asp Val Ser Ala Gly Asn Gly Ala Gly Ser			
	180	185	190
gta cag agg gtg gag atc ctg gag ggc cgc acc gag tgt gtg ctg agc			624
Val Gln Arg Val Glu Ile Leu Glu Gly Arg Thr Glu Cys Val Leu Ser			
	195	200	205
aac ctg cgg ggc cgg acg cgc tac acc ttc gcc gtc cgc gcg cgt atg			672
Asn Leu Arg Gly Arg Thr Arg Tyr Thr Phe Ala Val Arg Ala Arg Met			
	210	215	220
gct gag ccg agc ttc ggc ggc ttc tgg agc gcc tgg tcg gag cct gtg			720
Ala Glu Pro Ser Phe Gly Gly Phe Trp Ser Ala Trp Ser Glu Pro Val			
	225	230	235
tcg ctg ctg acg cct agc ggt gag gcc cca ggc ggg ggt gta gga gga			768
Ser Leu Leu Thr Pro Ser Gly Glu Ala Pro Gly Gly Gly Val Gly Gly			
	245	250	255
gcc agg gcg aat cac ggg gca agc cca ccg ccc tga			804
Ala Arg Ala Asn His Gly Ala Ser Pro Pro Pro			
	260	265	

<210> 11
 <211> 267
 <212> PRT
 <213> Homo sapiens

 <400> 11

Met	Asp	His	Leu	Gly	Ala	Ser	Leu	Trp	Pro	Gln	Val	Gly	Ser	Leu	Cys	1	5	10	15
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Pro	Lys	Phe	Glu	Ser	Lys	Ala	Ala	Leu	Leu	Ala	Ala	Arg	Gly	Pro	Glu	35	40	45	
Glu	Leu	Leu	Cys	Phe	Thr	Glu	Arg	Leu	Glu	Asp	Leu	Val	Cys	Phe	Trp	50	55	60	
Glu	Glu	Ala	Ala	Ser	Ala	Gly	Val	Gly	Pro	Gly	Asn	Tyr	Ser	Phe	Ser	65	70	75	80
Tyr	Gln	Leu	Glu	Asp	Glu	Pro	Trp	Lys	Leu	Cys	Arg	Leu	His	Gln	Ala	85	90	95	
Pro	Thr	Ala	Arg	Gly	Ala	Val	Arg	Phe	Trp	Cys	Ser	Leu	Pro	Thr	Ala	100	105	110	
Asp	Thr	Ser	Ser	Phe	Val	Pro	Leu	Glu	Leu	Arg	Val	Thr	Ala	Ala	Ser	115	120	125	
Gly	Ala	Pro	Arg	Tyr	His	Arg	Val	Ile	His	Ile	Asn	Glu	Val	Val	Leu	130	135	140	
Leu	Asp	Ala	Pro	Val	Gly	Leu	Val	Ala	Arg	Leu	Ala	Asp	Glu	Ser	Gly	145	150	155	160
His	Val	Val	Leu	Arg	Trp	Leu	Pro	Pro	Pro	Glu	Thr	Pro	Met	Thr	Ser	165	170	175	
His	Ile	Arg	Tyr	Glu	Val	Asp	Val	Ser	Ala	Gly	Asn	Gly	Ala	Gly	Ser	180	185	190	
Val	Gln	Arg	Val	Glu	Ile	Leu	Glu	Gly	Arg	Thr	Glu	Cys	Val	Leu	Ser	195	200	205	
Asn	Leu	Arg	Gly	Arg	Thr	Arg	Tyr	Thr	Phe	Ala	Val	Arg	Ala	Arg	Met	210	215	220	
Ala	Glu	Pro	Ser	Phe	Gly	Gly	Phe	Trp	Ser	Ala	Trp	Ser	Glu	Pro	Val	225	230	235	240

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Ala Arg Ala Asn His Gly Ala Ser Pro Pro Pro
260 265

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ctc ctg ctc gct ggg gcc gcc tgg gcg ccc ccg cct aac ctc ccg gac 96
Leu Leu Leu Ala Gly Ala Ala Trp Ala Pro Pro Pro Asn Leu Pro Asp
20 25 30
ccc aag ttc gag agc aaa gcg gcc ttg ctg gcg gcc cgg ggg ccc gaa 144
Pro Lys Phe Glu Ser Lys Ala Ala Leu Leu Ala Ala Arg Gly Pro Glu
35 40 45
gag ctt ctg tgc ttc acc gag cgg ttg gag gac ttg gtg tgt ttc tgg 192
Glu Leu Leu Cys Phe Thr Glu Arg Leu Glu Asp Leu Val Cys Phe Trp
50 55 60
gag gaa gcg gcg agc gct ggg gtg ggc ccg ggc aac tac agc ttc tcc 240
Glu Glu Ala Ala Ser Ala Gly Val Gly Pro Gly Asn Tyr Ser Phe Ser
65 70 75 80
tac cag ctc gag gat gag cca tgg aag ctg tgt cgc ctg cac cag gct 288
Tyr Gln Leu Glu Asp Glu Pro Trp Lys Leu Cys Arg Leu His Gln Ala
85 90 95
ccc acg gct cgt ggt gcg gtg cgc ttc tgg tgt tcg ctg cct aca gcc 336
Pro Thr Ala Arg Gly Ala Val Arg Phe Trp Cys Ser Leu Pro Thr Ala
100 105 110
gac acg tcg agc ttc gtg ccc cta gag ttg cgc gtc aca gca gcc tcc 384
Asp Thr Ser Ser Phe Val Pro Leu Glu Leu Arg Val Thr Ala Ala Ser
115 120 125
ggc gct ccg cga tat cac cgt gtc atc cac atc aat gaa gta gtg ctc 432
Gly Ala Pro Arg Tyr His Arg Val Ile His Ile Asn Glu Val Val Leu
130 135 140
cta gac gcc ccc gtg ggg ctg gtg gcg cgg ttg gct gac gag agc ggc 480
Leu Asp Ala Pro Val Gly Leu Val Ala Arg Leu Ala Asp Glu Ser Gly
145 150 155 160
cac gta gtg ttg cgc tgg ctc ccg ccg cct gag aca ccc atg acg tct 528

His	Val	Val	Leu	Arg	Trp	Leu	Pro	Pro	Pro	Glu	Thr	Pro	Met	Thr	Ser		
				165					170						175		
cac	atc	cgc	tac	gag	gtg	gac	gtc	tcg	gcc	ggc	aac	ggc	gca	ggg	agc	576	
His	Ile	Arg	Tyr	Glu	Val	Asp	Val	Ser	Ala	Gly	Asn	Gly	Ala	Gly	Ser		
			180					185					190				
gta	cag	agg	gtg	gag	atc	ctg	gag	ggc	cgc	acc	gag	tgt	gtg	ctg	agc	624	
Val	Gln	Arg	Val	Glu	Ile	Leu	Glu	Gly	Arg	Thr	Glu	Cys	Val	Leu	Ser		
		195					200					205					
aac	ctg	cgg	ggc	cgg	acg	cgc	tac	acc	ttc	gcc	gtc	cgc	gcg	cgt	atg	672	
Asn	Leu	Arg	Gly	Arg	Thr	Arg	Tyr	Thr	Phe	Ala	Val	Arg	Ala	Arg	Met		
	210					215					220						
gct	gag	ccg	agc	ttc	ggc	ggc	ttc	tgg	agc	gcc	tgg	tcg	gag	cct	gtg	720	
Ala	Glu	Pro	Ser	Phe	Gly	Gly	Phe	Trp	Ser	Ala	Trp	Ser	Glu	Pro	Val		
225					230					235					240		
tcg	ctg	ctg	acg	cct	agc	ggg	ctc	tga								747	
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1			5						10					15			
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			20					25					30				
Pro	Lys	Phe	Glu	Ser	Lys	Ala	Ala	Leu	Leu	Ala	Ala	Arg	Gly	Pro	Glu		
	35					40						45					
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50						55					60						
Glu	Glu	Ala	Ala	Ser	Ala	Gly	Val	Gly	Pro	Gly	Asn	Tyr	Ser	Phe	Ser		
65					70					75					80		
Tyr	Gln	Leu	Glu	Asp	Glu	Pro	Trp	Lys	Leu	Cys	Arg	Leu	His	Gln	Ala		
				85					90					95			
Pro	Thr	Ala	Arg	Gly	Ala	Val	Arg	Phe	Trp	Cys	Ser	Leu	Pro	Thr	Ala		
			100					105					110				
Asp	Thr	Ser	Ser	Phe	Val	Pro	Leu	Glu	Leu	Arg	Val	Thr	Ala	Ala	Ser		
		115					120					125					

Gly Ala Pro Arg Tyr His Arg Val Ile His Ile Asn Glu Val Val Leu
 130 135 140

Leu Asp Ala Pro Val Gly Leu Val Ala Arg Leu Ala Asp Glu Ser Gly
 145 150 155 160

His Val Val Leu Arg Trp Leu Pro Pro Pro Glu Thr Pro Met Thr Ser
 165 170 175

His Ile Arg Tyr Glu Val Asp Val Ser Ala Gly Asn Gly Ala Gly Ser
 180 185 190

Val Gln Arg Val Glu Ile Leu Glu Gly Arg Thr Glu Cys Val Leu Ser
 195 200 205

Asn Leu Arg Gly Arg Thr Arg Tyr Thr Phe Ala Val Arg Ala Arg Met
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21